

## **P16 – Epigenetic analysis reveals differentially methylated regions between cultivated and wild grapevines**

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### **Abstract**

**Grapevine domestication** has traditionally been based in clonal propagation, with the aim of enhancing and selecting grapes traits (like fruit size or berry sugar content) and reducing heterogeneity in the vineyard. Due to the domestication process, *Vitis vinifera* L. was separated in two subspecies based on morphological differences: *Vitis vinifera* ssp *sylvestris* and *Vitis vinifera* ssp *vinifera*, which differences concentrate in reproductive phenotype and environmental adaptations. These phenotypic differences could be explained both by the selection of genetic and **epigenetic variation** occurred during species evolution. The contribution of genetic variability towards the observed phenotypic diversity and plasticity of cultivated and wild *V. vinifera*, has been extensively studied. However, very little effort has been directed at the selection of epialleles during grapevine's domestication. To explore the **epigenomic differences between the two subspecies**, we characterized the methylome across 8 wild accessions (WT) of *Vitis vinifera* ssp *sylvestris* and 10 cultivated varieties (CV) of *Vitis vinifera* L. ssp *vinifera* using a reduced-representation genome sequencing approach (**epiGBS**). Genome-wide analysis of differentially methylated regions (DMRs) identified a total of 9955 DMRs, of which, 7793 were hypermethylated and 2162 hypomethylated in cultivated varieties in comparison to wild accessions. Additionally, study of the location of DMRs in relation to genomic features, showed **higher DNA methylation levels in intergenic regions in WT than in CV in all methylation contexts (i.e., CG, CHG, and CHH)**. Conversely, we found a **higher percentage of methylated regions (in all contexts) in gene promoters of the CV group** (and different methylation rates in **intron** and **exon** between CV and WT groups). The results suggested that, although the methylome of CV and WT groups were modelled under the same environmental conditions, we showed that regions harboring polymorphic methylation could contribute to functionally relevant phenotypic variation across them.

**Keywords:** Epigenetics, methylome, domestication, wild, cultivar, grapevine, DMR